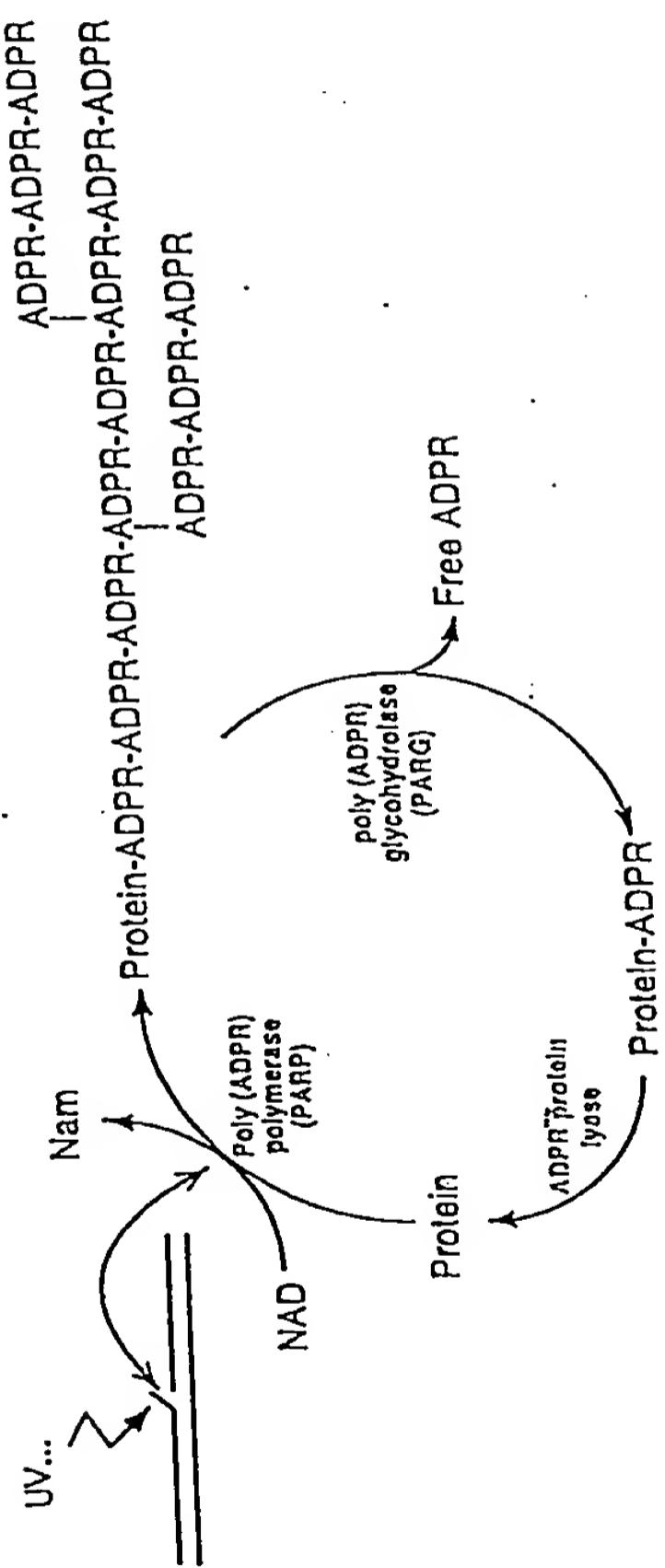
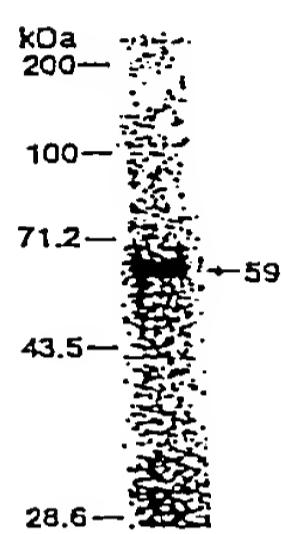


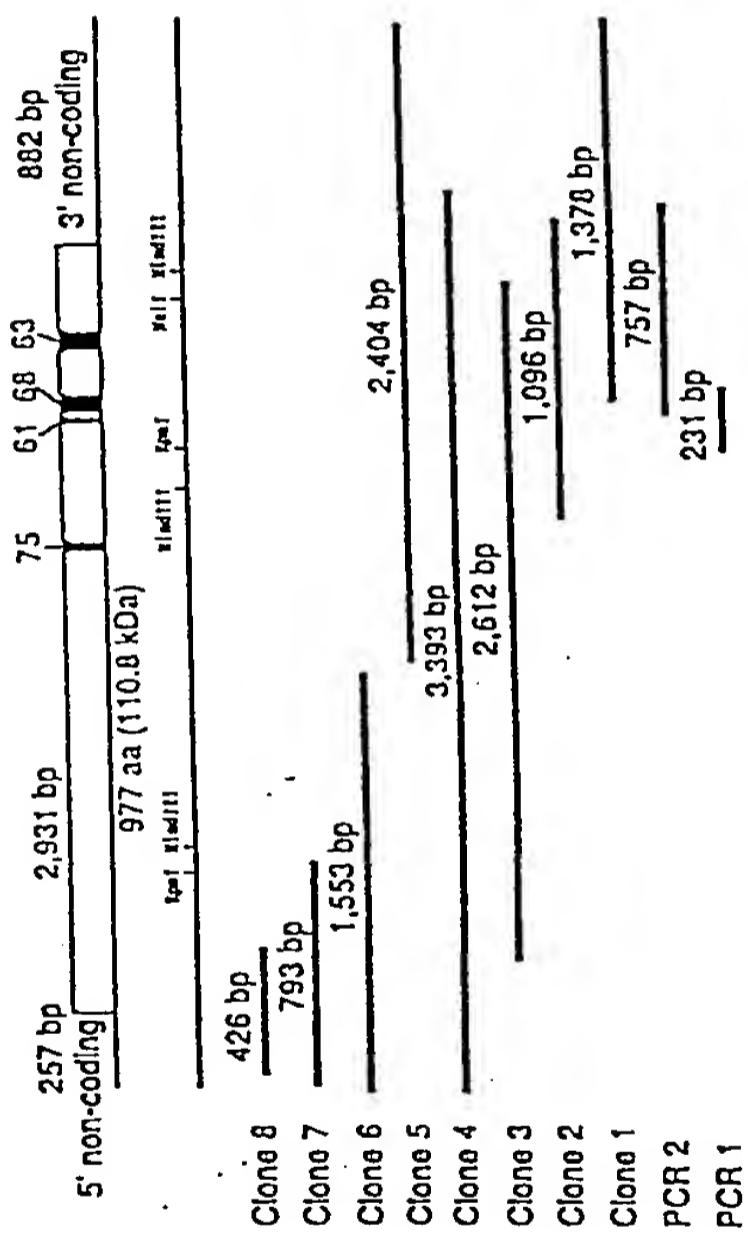
# FIGURE 1



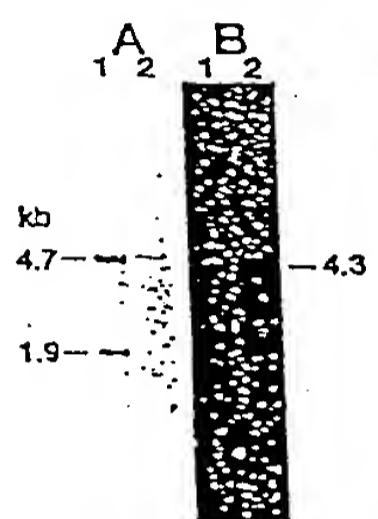
## FIGURE 2



## FIGURE 3



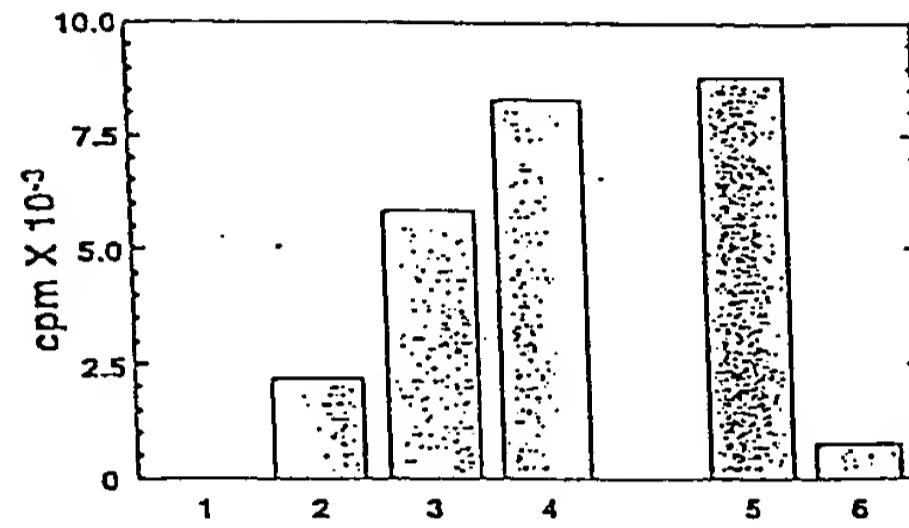
## FIGURE 4



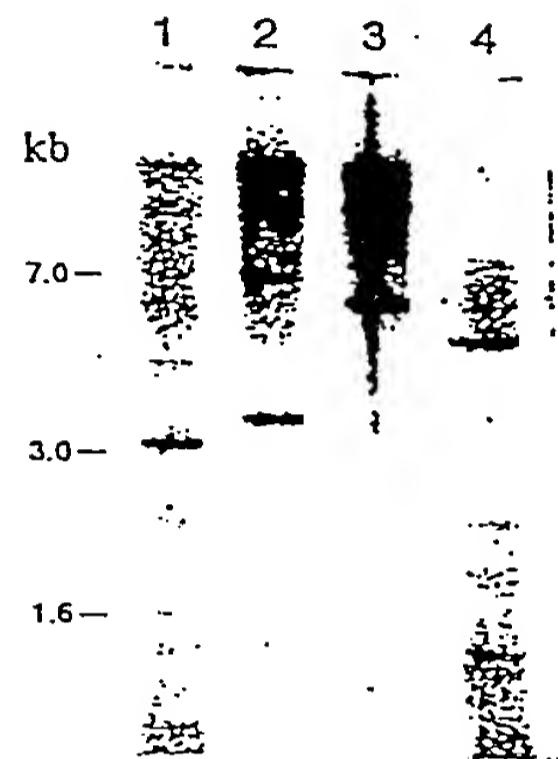
bPARG (422) ED . . . KRKEQCEMKHQRT . . RKİPKYI PPH SEQ ID NO: 19  
hPARG (421) ED . . . RRKEQWETKHQRT . . RKİPKYVPPH SEQ ID NO: 20  
mPARG (413) ED . . . RRKEQCEVRHQRT . . RKİPKYI PPN SEQ ID NO: 21  
cEPARG (29) HQVPTMKRKLTEHGNNTESLLIKEEPEPKS SEQ ID NO: 22

hPARP (205) EG . . . KRKG D. EVDG. VDEVAKKKSKKEKDK SEQ ID NO: 23  
mPARP (205) EG . . . KRKG D. EVDG. TDEVAKKKSRKETDK SEQ ID NO: 24  
bPARP (208) EG . . . KRKG D. EVDG. IDEVTKKKS KKEKDK SEQ ID NO: 25  
aPARP (205) EG . . . KRKG E. EVDG. . NVVAKKKSRKEKEK SEQ ID NO: 26  
XI PARP (204) EG . . . KRKAD. EVDG. HSAATKKKTI KKEKEK SEQ ID NO: 27  
DmPARP (202) EELPDTKRAKM. ELSDTNEEGEKKQR . . . . SEQ ID NO: 28  
SpPARP (205) EGVSSAKKAKI. EKIDEEDAASIKELTEKIKK SEQ ID NO: 29

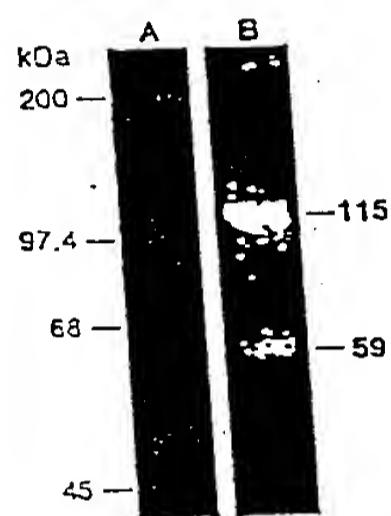
## FIGURE 6



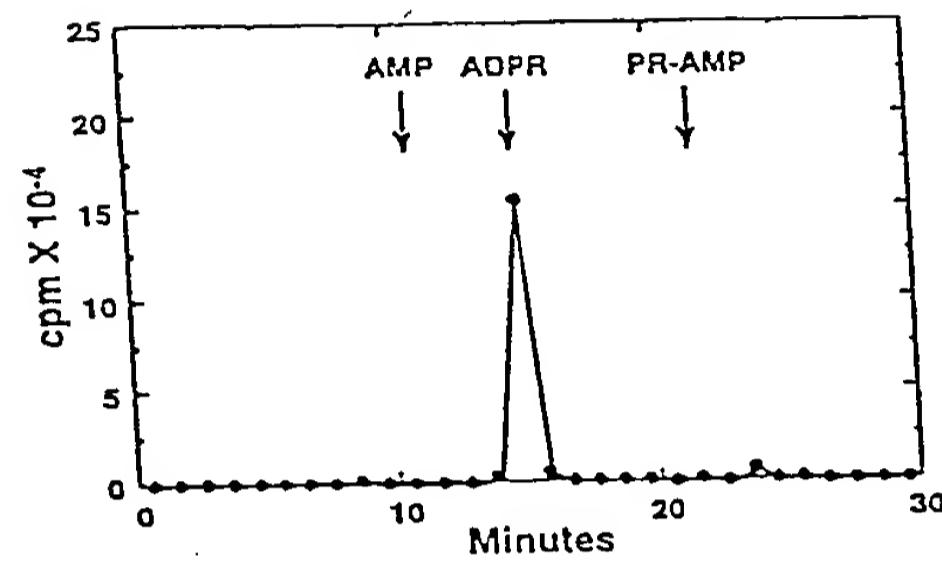
## FIGURE 7



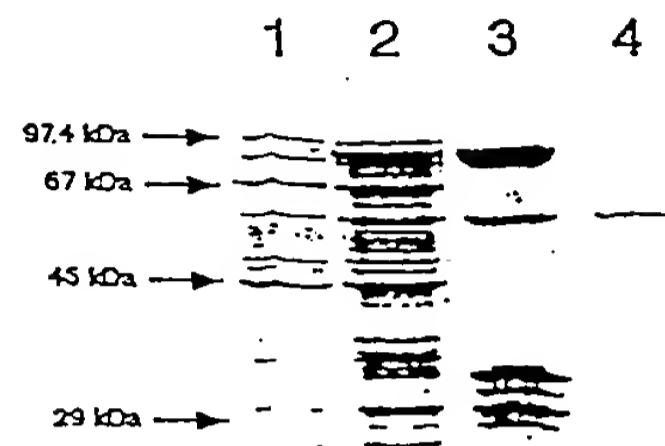
## FIGURE 8



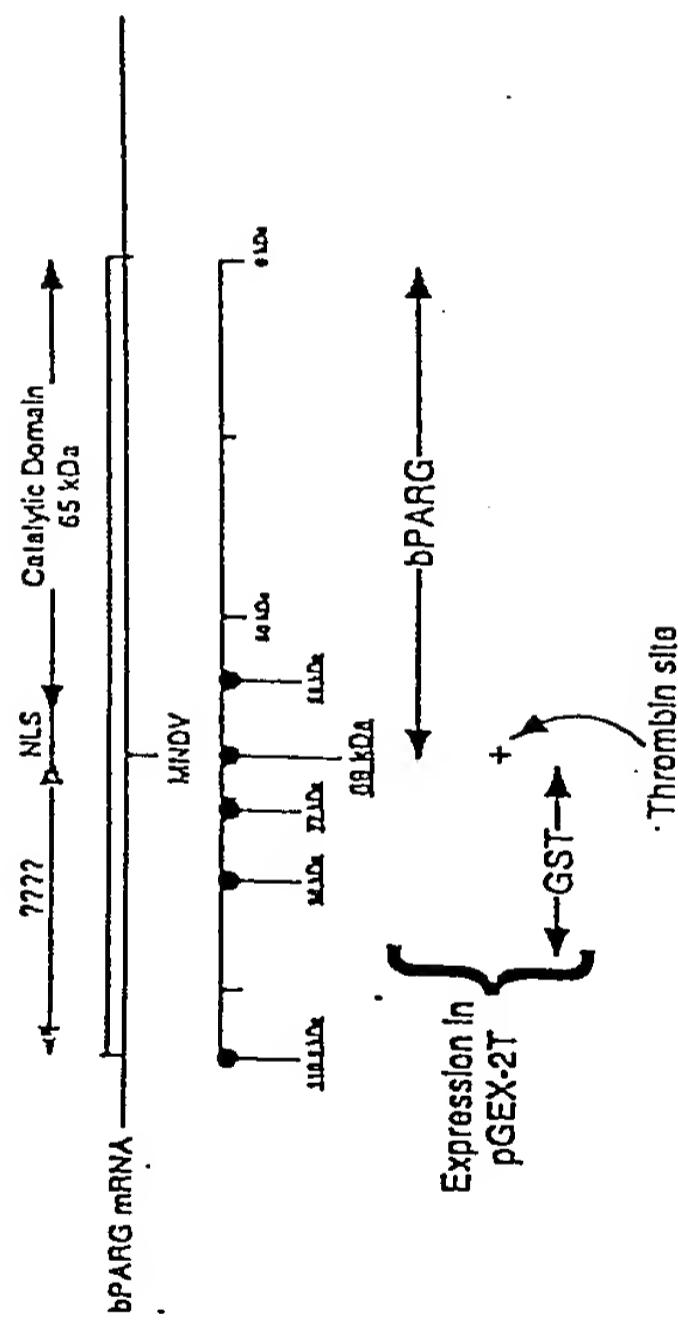
# FIGURE 9



## FIGURE 10

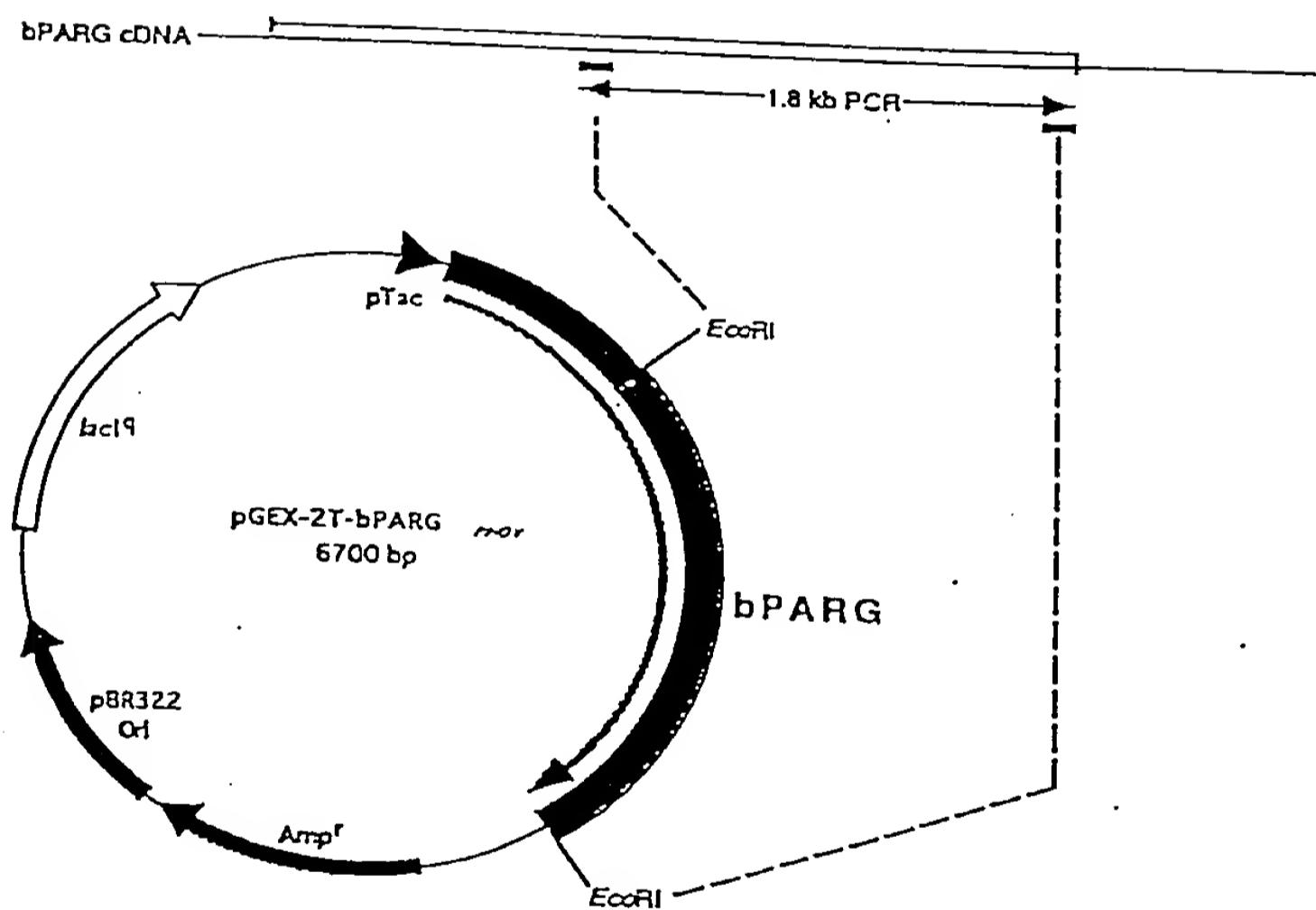


## FIGURE 11

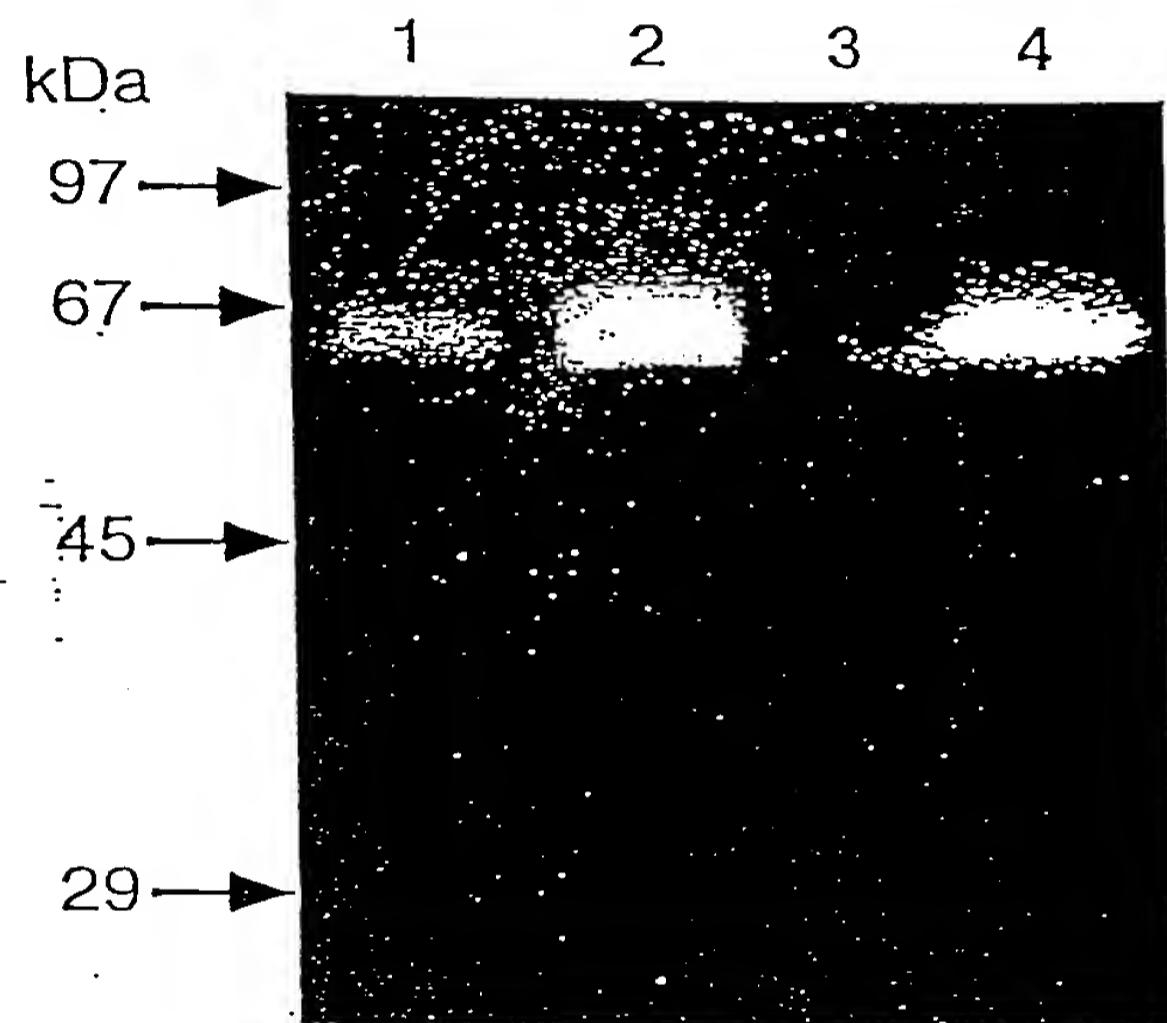


## FIGURE 12

Design of expression vector pGEX-2T-bPARG

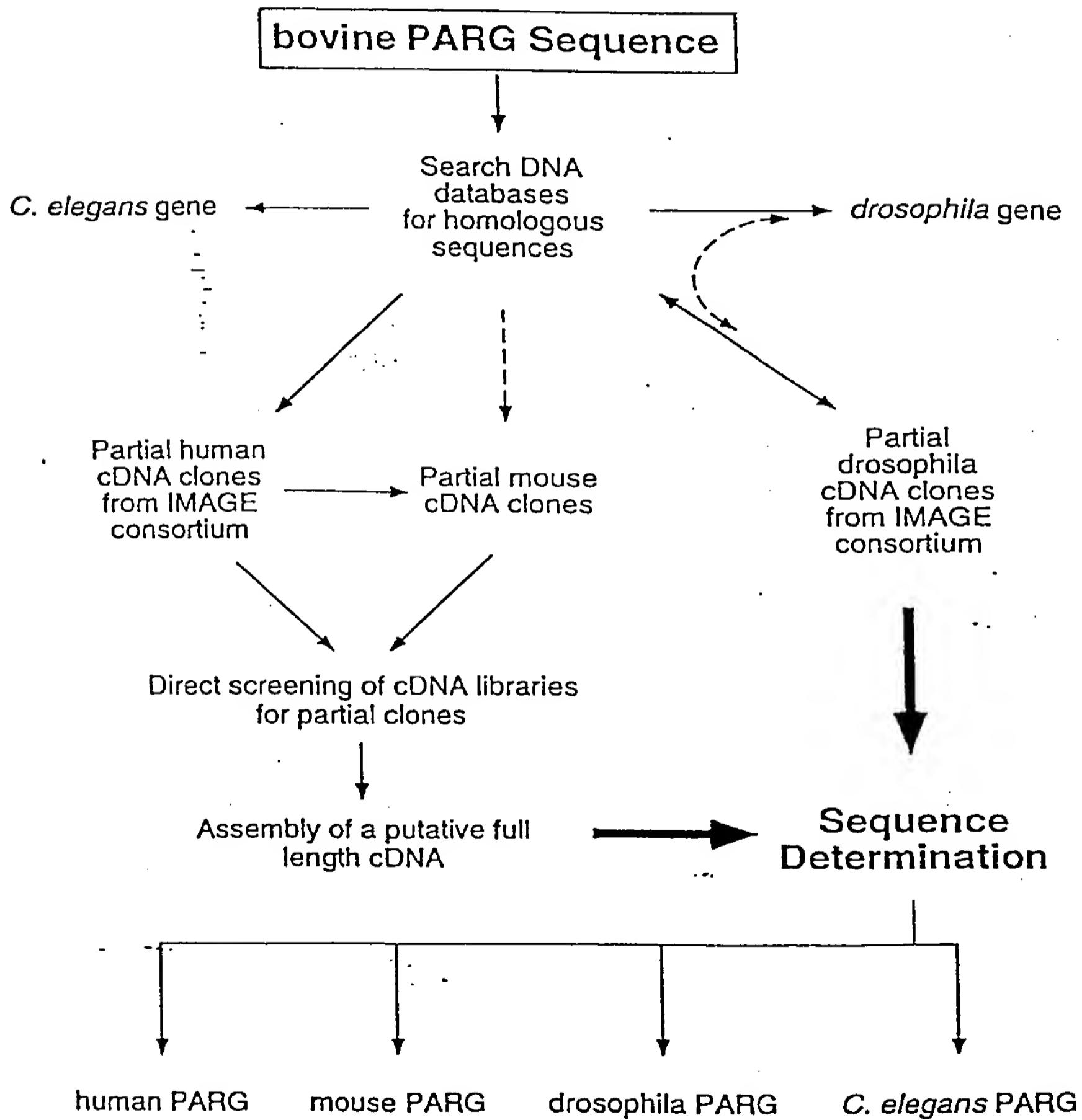


**FIGURE 13**

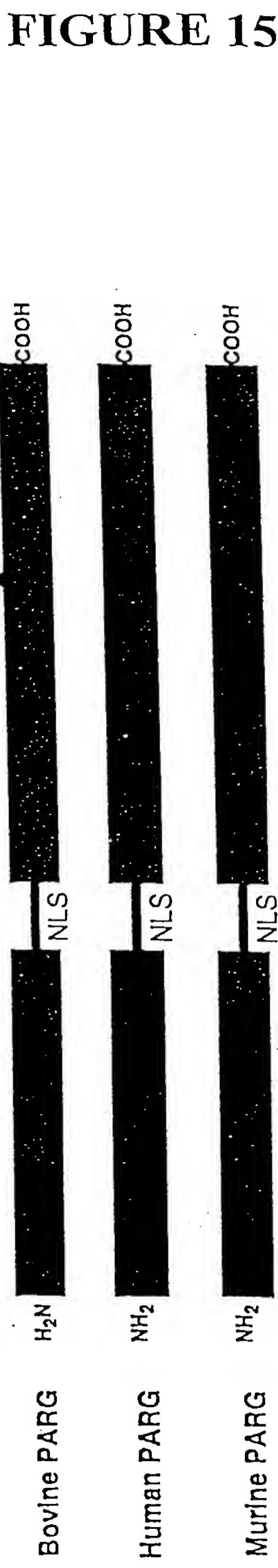


**FIGURE 14**

## Strategy to Obtain Homologous PARG Sequences



# Domain Organization of PARGs



# FIGURE 16

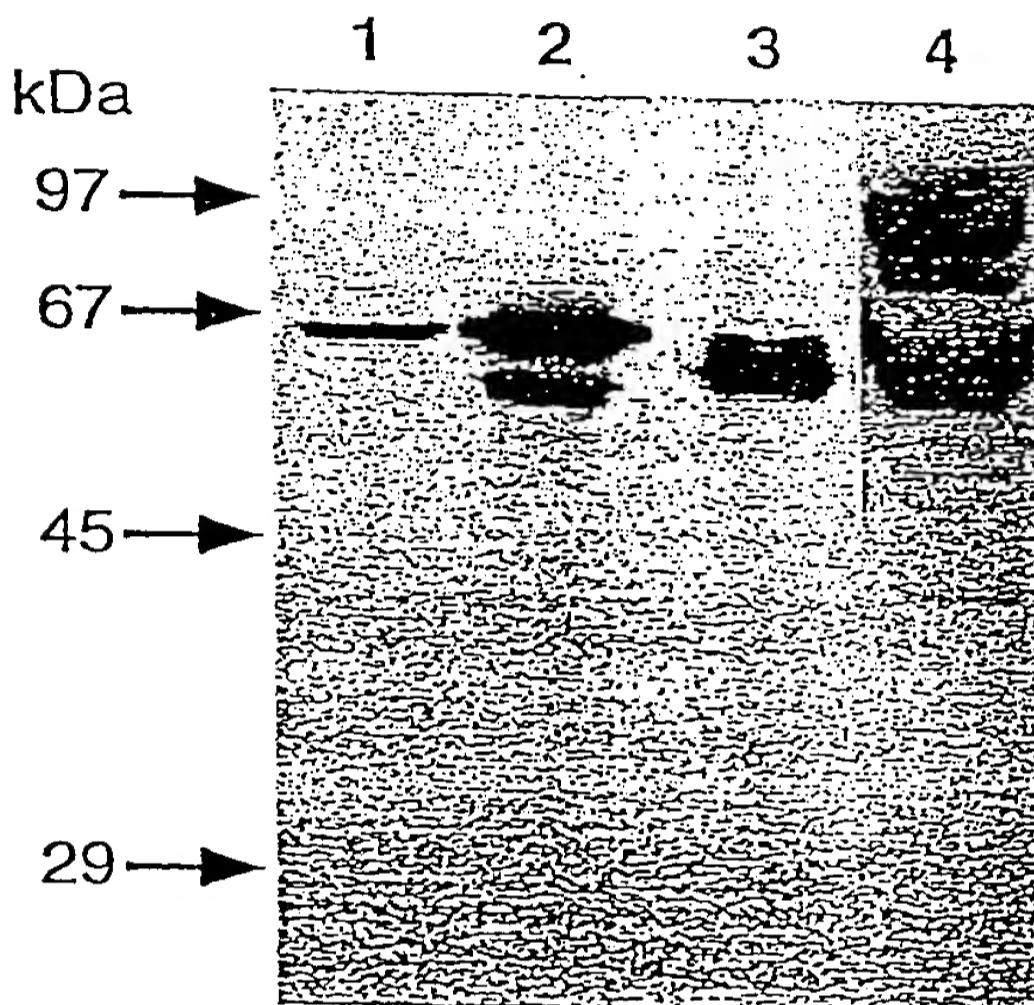
## Multiple Alignment of Amino Acid Sequences of PARG from Different Species

```

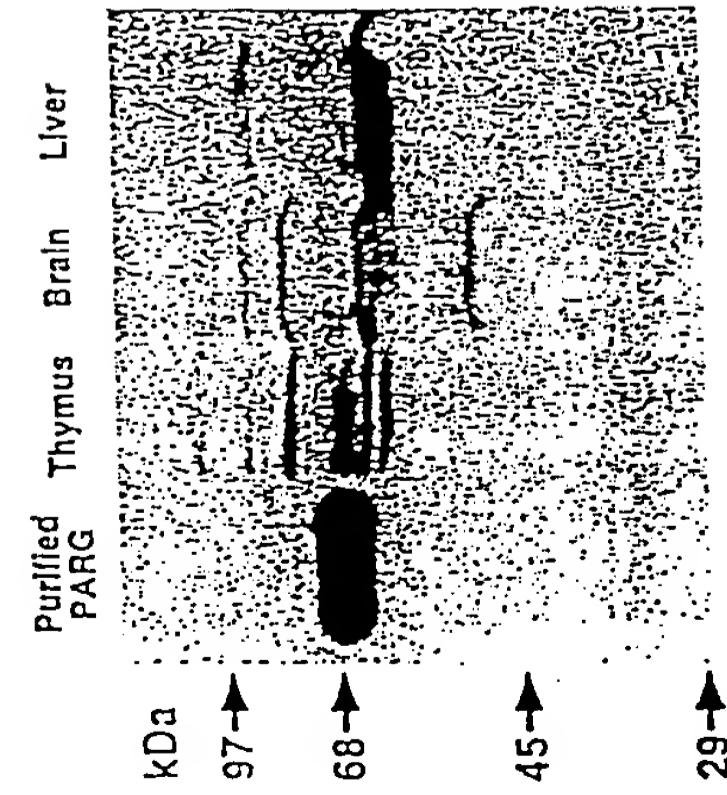
parg      1 MSAGPGCERPCTKPRWDAATSPPARSDARSFPGRQRRLVLDSDKDAPVQFRVPPSSSGCALGRAGQHRSATSLVFKQRTITSWNMDTKGIKTVESLSHK
parg      1 MHAGPGCERPCTKATRWGAATTs. PAASDARSFPGRQRRLVLDSDKDAPVQFRVPPSSPACVPGQAGQHRSATSLVFKQRTITSWNMDTKGIKTAESLSK
parg      1 MSAGPGWEPCTKA.RWGAGTSAPTASDERSFPGRQRRLVLDSDKDAPVQFRVPPSSPACVSGRAGPHRGNATSFVFQKQTITTWMDTKGPKTAESE...SK
parg      1 -----
parg      1 -----
parg      101 EHHNTREESMNSSVQKDHFYQHNMKLENVSQLGFDKSPVEKGQTQLKQEQTAAAMCKHQNEGPHSERLLESSEPPAVTLVPEQFSNAHVQDQSSPKDDHESDT
parg      100 EHHNTRIESMNSSVQKDHFYQHNMVKLVNVSQLSDLKSLTEKSTQILNQHQTAAAMCKHQNEGKHTEQLLESSEPPQTVTLVPEQFSNAHVDRSPQNDDHESDT
parg      97 EHHNTRIDSMNSSVQKDHFYQHNMVKLVNVQPLNLDSPTERSSQYLNQQQTASVCKHQNEGKHAEQQLLASSEPPAGTPLPKQLSHANIGQSPHTDDESDT
parg      1 -----
parg      1 -----
parg      201 NSEESRDHQQFLTHVKL...ANAKQTMEDEQGREARSHQKCGKACHPAEACAGCCQQKEETDVVSESPLSDTGSEDVGTLKNAIRLNQESSLGNSSPFKK
parg      200 DSEEHDRDNQQFLTTVKL...ANAKQTTEDEHAREAKSHQKCSKSCEPGEDCASCQQDIEIDVVPKSPLSDVGSEDVGTSKHDNKLIRQESCLGNSSPFKK
parg      197 DEEEHDRDNQQFLTPIKL...ANTKPTVGDQ...ARSHCKCGSRQSVKDCTGCQQKEEVVDVLPESPLSDVGAEDIGTGPKHDKLGTQGESSLGDSPPFKK
parg      1 -----
parg      23 VGVGFARHQVPTMKRRKLTENHNTTESKEDPEEPKSRDVFVSSQSSDESQEDSAEHPEIAKEVSENCENLTELKISNIESLDNVTERSEHTLDH...HK
parg      298 ESEPESPMDVDNSKNSCQDSEADEETSPGFDE.QEDSSSAQTAAKPSRFQPREADTELRRRSSAKGGEIRLHFQEGGESRAGMN.DVHAKRPGSTSSLN
parg      297 ESEPESPMDVDNSKNSCQDSEADEETSPGFDE.QEDGSSSQTAANKPSRFQARDADIEFRKRISTKGGEVRLEFQPEGGESRTGMN.DLHAKLPGNISSLN
parg      291 ESEPESPMDVDNSRSCQDSEADEETSPVFDE.QDDRSS.QTAHKLSSCQAREADGDLRKRYLTKGSEVRLEFQFE.GENNAGTS.DLHAKPSGNSSSLN
parg      1 -----
parg      119 STEPME.DVNMRKSHIDVAINSDDEDELVLEENHKEMRDGEQVQQQLS..QDLFADDQELIEYPGIMKDITDSEVETAQKMEMIEETEADSTPYG
parg      396 VECRNSKQHGRKDSKITDHFMRVPKAEDRKKEQCEMKHQRTERKIPYIIPPHLSPDKWLGTPIEEM..RRMPRCGIRLPLRPSANHTVTIRV DLLRIG
parg      395 VECRNSKQHGRKDSKITDHLMRLPKAEDRKKEQWETKHZQRTERKIPYIIPPHLSPDKWLGTPIEEM..RRMPRCGIRLPLRPSANHTVTIRV DLLRAG
parg      387 VECRNSKQHGRKDSKITDHFMRIKSKEDDRRKEQCEVRHQRTERKIPYIIPPHLSPDKWLGTPIEEM..RRMPRCGIRLPLRPSASHTVTIRV DLLRAG
parg      32 ...TNRLGK...ALCLNCARMSKSPDGCGISEKIE....TEEE.PENLANSL..DDSWRGVSMEAHRNRQPFELNPPVTAGNLHRVMQLPIRET.
parg      216 EDASKATKTVRTSSSF..LSTVSTCEAPAKGRAMIQKELEKHVIAFTEGNLT....LQPDLNKVDPDRNRY.CTIPNFPASQG..KLRED.NRYG
parg      494 EVPK.PFPTEPKDLWDNHKHKVMPCEQNLIPVEDENGE.RAAGSRWELIQTALLNRLTRPQHLKDAILKYNVAISKWDFTALIDFWDKVLEEAQHLY
parg      493 EVPK.PFPTEPKDLWDNHKHKVMPCEQNLIPVEDENGE.RTAGSRWELIQTALLNRLTRPQHLKDAILKYNVAISKWDFTALIDFWDKVLEEAQHLY
parg      485 EVPK.PFPTEPKDLWDNHKHKVMPCEQNLIPVEDENGE.RTAGSRWELIQTALLNRLTRPQHLKDAILKYNVAISKWDFTALIDFWDKVLEEAQHLY
parg      115 .PPR.PIKSPGK..WDSEEVRLPCAPESKIPRENPDGS.TTIDFRNEMIERALLQPIKTCEEELQAAIISINTTIRDQWHFRALQQLDEELDESETRVFF
parg      303 ..PKIVLPQRWR.E.FDSRGRR...RDSYFYFKRKLDGYLKCYKTTGYFMVGLH.....HMWE..FDPDITYK...LPAL.EHYIKEMSELVGRBEEV
parg      592 QSILPDMVKIALCLPNICTQPIPLLKQKMHESITMSQEIQIASLLAHAPPCTFPRRNA.KMKSEISSYPDINFHLFEGRSSRKPEKLKTLFCYFRRV..T
parg      591 QSILPDMVKIALCLPNICTQPIPLLKQKMHESITMSQEIQIASLLAHAPPCTFPRRNA.KMKSEISSYPDINFHLFEGRSSRKPEKLKTLFCYFRRV..T
parg      583 QSILPDMVKIALCLPNICTQPIPLLKQKMHESITMSQEIQIASLLAHAPPCTFPRRNA.KMKSEISSYPDINFHLFEGRSSRKPEKLKTLFCYFRRV..T
parg      210 EDLLPRIIRLALRLPDLIQSPVPLKHHKMASLSSLQQQISCLLAAFLCTFPRRNLTLRKSEYSTFPDINFHLFEGRSSRKPEKLKTLFCYFRRVCP
parg      384 LEKFARVARIAKTAEDILPERIYRLVGDVE.SATLSHKQCAALVARMFA.....RPDSPFS.....FCRILSSDKSICVERLKFLFTYF.....
parg      689 EKK...PTGLVTFTRQS.L.ED.F.PEWERC KLL..TRLHVTIETGTIEGHGQGMLQVDFAHRFVGGGVTSAGLVQEIRFLINPELIVSRLFTEVLDH
parg      688 EKK...PTGLVTFTRQS.L.ED.F.PEWERC KPL..TRLHVTIETGTIEGHGQGMLQVDFAHRFVGGGVTSAGLVQEIRFLINPELIVSRLFTEVLDH
parg      680 EKK...PTGLVTFTRQS.L.ED.F.PEWERC KPL..TRLHVTIETGTIEGHGQGMLQVDFAHRFVGGGVTSAGLVQEIRFLINPELIVSRLFTEVLDH
parg      310 ERDASNVPVTGVVTFVRRSGLPKE.L.IDWSQSAAPLGDVPLHVDAGTIKDEGIGLLQVDFANKYLGGGVLGEGCVQEBIRFVICPELLVGKLFTECLRP
parg      463 DKMSMDPPDGAVSF.RLTKMDKDTFNEEW.KDKKLRSLPEVEFFFDEMIEDTAL.CTQVDFANEHLLGGGVLHEGSVQEIRFLMCPEMMVGMLCKMKQ
parg      779 NECLIITGTQISETGYAETYRWA....RSHEDRSE.RDDWQRRTTEIVAI DALHFR.RYLD...QFVPEKIRRELKAYCGLRPGVSSENLSAVA
parg      778 NECLIITGTQISETGYAETYRWS....RSEEDGSE.RDDCERRCTEIVAI DALHFR.RYLD...QFVPEKMRRLKAYCGLRPGVSSENLSAVA
parg      770 NECLIITGTQISETGYAETYRWA....RSHEDGSE.KDDWQRRTCTEIVAI DALHFR.RYLD...QFVPEKVRRELKAYCGLRPGVSSENLSAVA
parg      408 FEALVMLGAERIISNYITGYAGSFENS....GNFEDSTP.RDSSGRRQTAIVAI DALHFA.QSHE...QIREDLMERELNKAYIGFVEWMVTPP..PGVA
parg      560 LEAISIVGAYVSSITGYGHTLKWABLQPNHSRQNTNEPRDRFGRLRVTIAIDAILFKGSKLDCQTEQLNKAII REMKKASIGFMSQGPKFTHIP.IV
parg      868 TGNNGCGAFGGDARLKALIQILAAAARVDVYFTFGDSELMRDIYSMHTFLTERKLTVGE.VIKLLLRYIHEECRNCSTPGP....DIKLYPPFIHA
parg      867 TGNNGCGAFGGDARLKALIQILAAAARVDVYFTFGDSELMRDIYSMHTFLTERKLTVGD.VIKLLLRYIHEECRNCSTPGP....DIKLYPPFIHA
parg      859 TGNNGCGAFGGDARLKALIQILAAAARVDVYFTFGDSELMRDIYSMHTFLTERKLTVGD.VIKLLLRYIHEECRNCSTPGP....DIKLYPPFIHA
parg      495 TGNNGCGAFGGDSILKALLQLMVCAQLGRPLAYTFTGHNVERFDDFHEMWLLFRNDGTTVQQ.LWS.ILRSYSRLIKEKSSKEPRENKASKKLYDFI...
parg      659 TGNNGCGAFNGDKPLKFIQVIAGVADRPLFHCFSFGEPELAACKKIIERMKQKDVTLGKSCPSIFS-----
parg      961 VESCTQTTNQPGQRTGA-----
parg      960 VESCAETADHSGQRTGT-----
parg      952 VESSAETTDMPGQKAGT-----
parg      590 KEELKKVVRDVPGEGASAAGSSRVAGLGEVKSETSAKSSPELNKOPARPOITITQOSTDLLPAQLSQDNSNSSEDQALLMLSDDDEANAMMERAASLEAKS
parg      727 -----
parg      978 -----
parg      977 -----
parg      969 -----
parg      690 SVEISNSSTSCTSSTATKSMGSGGRQLSLLMHDTEYKGSASKPRKSPNCSSAKSAKSRAEIDVTDKDEKDDIVD
parg      727 -----

```

**FIGURE 17**



A  
Bovine Tissue



Cell Extracts

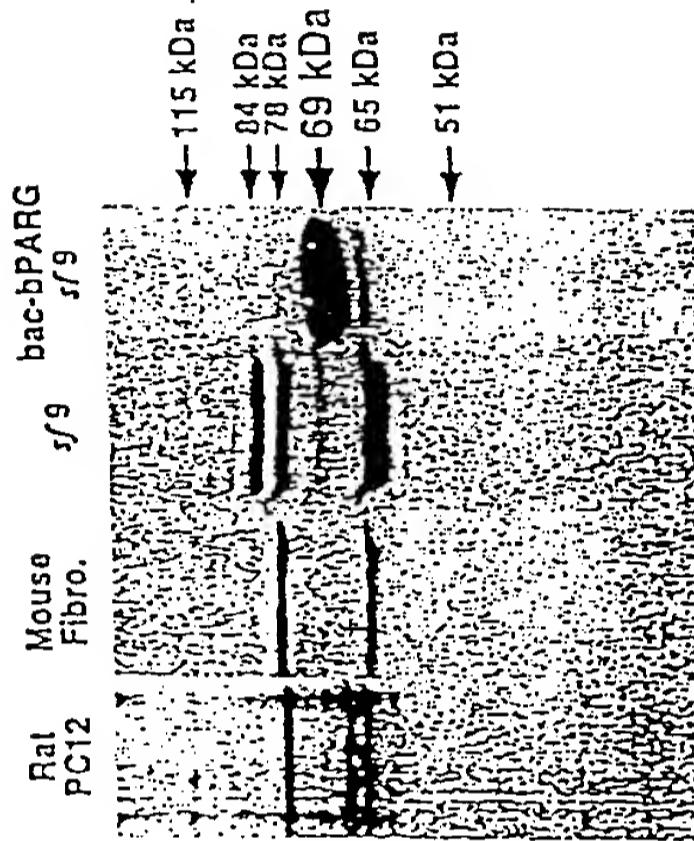
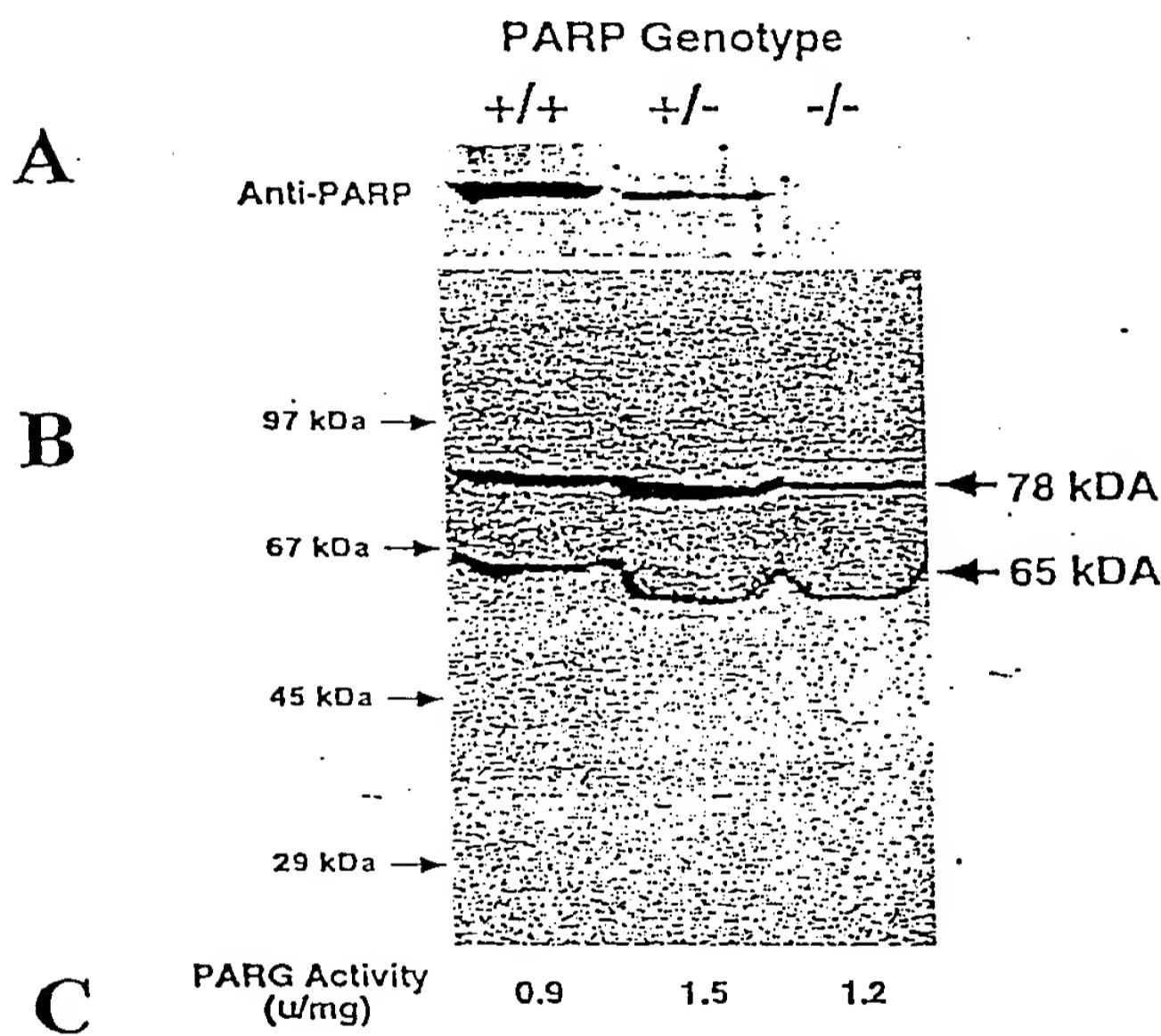


FIGURE 18

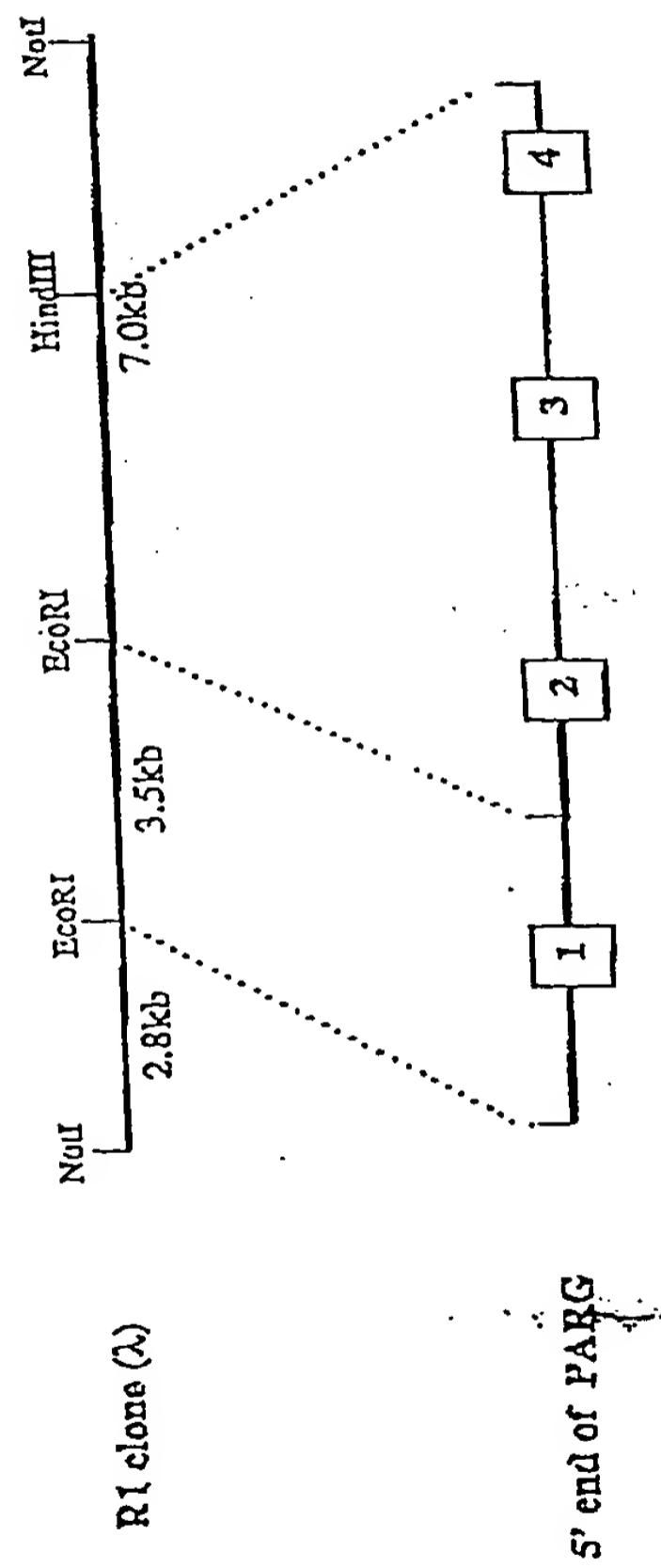
## FIGURE 19

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**FIGURE 20**

**Genomic cloning of the PARG gene**



**FIGURE 21**

Targeted ES cell clones

